

1

## SEQUENCE LISTING

<110> The Board of Control of  
 Michigan Technological University et al.  
 Sel A  
 <120> GENETIC ENGINEERING OF LIGNIN BIOSYNTHESIS IN PLANTS  
 <130> 881.003WO1  
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 Val Leu Glu Asn Leu Ser Lys His Ser Ser Lys Pro Cys Leu Ile Asn  
 30 35 40  
 ggc gcg aat gga gat gtc tac acc tat gct gat gtt gag ctc aca gca 256  
 Gly Ala Asn Gly Asp Val Tyr Thr Tyr Ala Asp Val Glu Leu Thr Ala  
 45 50 55  
 aga aga gtt gct tct ggt ctg aac aag att ggt att caa caa ggt gac 304  
 Arg Arg Val Ala Ser Gly Leu Asn Lys Ile Gly Ile Gln Gln Gly Asp  
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 Val Ile Met Leu Phe Leu Pro Ser Ser Pro Glu Phe Val Leu Ala Phe  
 75 80 85 90  
 cta ggc gct tca cac aga ggt gcc atg atc act gct gcc aat cct ttc 400  
 Leu Gly Ala Ser His Arg Gly Ala Met Ile Thr Ala Ala Asn Pro Phe  
 95 100 105  
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 Ser Thr Pro Ala Glu Leu Ala Lys His Ala Lys Ala Ser Arg Ala Lys

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cga gaa agt gat gtt aag gtc atg tgc gtc gac tct gcc ccg gac ggt Arg Glu Ser Asp Val Lys Val Met Cys Val Asp Ser Ala Pro Asp Gly 140 145 150			544
gct tca ctt ttc aga gct cac aca cag gca gac gaa aat gaa gtc cct Ala Ser Leu Phe Arg Ala His Thr Gln Ala Asp Glu Asn Glu Val Pro 155 160 165 170			592
cag gtc gac att agt cct gat gtc gta gca ttg cct tat tca tca Gln Val Asp Ile Ser Pro Asp Asp Val Val Ala Leu Pro Tyr Ser Ser 175 180 185			640
ggg act aca ggg ttg cca aaa ggg gtc atg tta acg cac aaa ggg cta Gly Thr Thr Gly Leu Pro Lys Gly Val Met Leu Thr His Lys Gly Leu 190 195 200			688
ata acc agt gtg gct caa cag gta gat gga gac aat cct aac ctg tat Ile Thr Ser Val Ala Gln Gln Val Asp Gly Asp Asn Pro Asn Leu Tyr 205 210 215			736
ttt cac agt gaa gat gtg att ctg tgt gtg ctt cct atg ttc cat atc Phe His Ser Glu Asp Val Ile Leu Cys Val Leu Pro Met Phe His Ile 220 225 230			784
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att ttg ata atg cca aag ttt gag att ggt tct ttg ctg gga ttg att Ile Leu Ile Met Pro Lys Phe Glu Ile Gly Ser Leu Leu Gly Leu Ile 255 260 265			880
gag aag tac aag gta tct ata gca cca gtt gtt cca cct gtg atg atg Glu Lys Tyr Lys Val Ser Ile Ala Pro Val Val Pro Pro Val Met Met 270 275 280			928
gca att gct aag tca cct gat ctt gac aag cat gac ctg tct tct ttg Ala Ile Ala Lys Ser Pro Asp Leu Asp Lys His Asp Leu Ser Ser Leu 285 290 295			976
agg atg ata aaa tct gga ggg gct cca ttg ggc aag gaa ctt gaa gat Arg Met Ile Lys Ser Gly Gly Ala Pro Leu Gly Lys Glu Leu Glu Asp 300 305 310			1024
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aac cag cct ggt gag atc tgc atc cgg ggt gat cag atc atg aaa gga	1264
Asn Gln Pro Gly Glu Ile Cys Ile Arg Gly Asp Gln Ile Met Lys Gly	
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Tyr Leu Asn Asp Pro Glu Ala Thr Ser Arg Thr Ile Asp Lys Glu Gly	
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Trp Leu His Thr Gly Asp Ile Gly Tyr Ile Asp Asp Asp Asp Glu Leu	
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Phe Ile Val Asp Arg Leu Lys Glu Leu Ile Lys Tyr Lys Gly Phe Gln	
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gtt gct cct act gaa ctc gaa gct ttg tta ata gcc cat cca gag ata	1456
Val Ala Pro Thr Glu Leu Glu Ala Leu Leu Ile Ala His Pro Glu Ile	
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Ser Asp Ala Ala Val Val Gly Leu Lys Asp Glu Asp Ala Gly Glu Val	
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Glu Ile Lys Gln Tyr Ile Ser Lys Gln Val Ile Phe Tyr Lys Arg Ile	
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aaa cga gtt ttc ttc att gaa gca att ccc aag gca cca tca ggc aag	1648
Lys Arg Val Phe Phe Ile Glu Ala Ile Pro Lys Ala Pro Ser Gly Lys	
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atc ctg agg aag aat ctg aaa gag aag ttg cca ggc ata taactgaaga	1697
Ile Leu Arg Lys Asn Leu Lys Glu Lys Leu Pro Gly Ile	
525 530 535	
tgttactgaa catttaaccc tctgtcttat ttcttaata cttgcgaatc attgttagtgt	1757
tgaaccaagc atgcttgaa aagacacgta cccaacgta gacagttact gttccttagta	1817
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Lys His Ser Ser Lys Pro Cys Leu Ile Asn Gly Ala Asn Gly Asp Val  
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Tyr Thr Tyr Ala Asp Val Glu Leu Thr Ala Arg Arg Val Ala Ser Gly  
50 55 60  
Leu Asn Lys Ile Gly Ile Gln Gln Gly Asp Val Ile Met Leu Phe Leu  
65 70 75 80  
Pro Ser Ser Pro Glu Phe Val Leu Ala Phe Leu Gly Ala Ser His Arg  
85 90 95  
Gly Ala Met Ile Thr Ala Ala Asn Pro Phe Ser Thr Pro Ala Glu Leu  
100 105 110  
Ala Lys His Ala Lys Ala Ser Arg Ala Lys Leu Leu Ile Thr Gln Ala  
115 120 125  
Cys Tyr Tyr Glu Lys Val Lys Asp Phe Ala Arg Glu Ser Asp Val Lys  
130 135 140  
Val Met Cys Val Asp Ser Ala Pro Asp Gly Ala Ser Leu Phe Arg Ala  
145 150 155 160  
His Thr Gln Ala Asp Glu Asn Glu Val Pro Gln Val Asp Ile Ser Pro  
165 170 175  
Asp Asp Val Val Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro  
180 185 190  
Lys Gly Val Met Leu Thr His Lys Gly Leu Ile Thr Ser Val Ala Gln  
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Gln Val Asp Gly Asp Asn Pro Asn Leu Tyr Phe His Ser Glu Asp Val  
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Ile Leu Cys Val Leu Pro Met Phe His Ile Tyr Ala Leu Asn Ser Met  
225 230 235 240  
Met Leu Cys Gly Leu Arg Val Gly Ala Ser Ile Leu Ile Met Pro Lys  
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Phe Glu Ile Gly Ser Leu Leu Gly Leu Ile Glu Lys Tyr Lys Val Ser  
260 265 270  
Ile Ala Pro Val Val Pro Pro Val Met Met Ala Ile Ala Lys Ser Pro  
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Asp Leu Asp Lys His Asp Leu Ser Ser Leu Arg Met Ile Lys Ser Gly  
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Gly Ala Pro Leu Gly Lys Glu Leu Glu Asp Thr Val Arg Ala Lys Phe  
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Pro Gln Ala Arg Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro  
325 330 335  
Val Leu Ala Met Cys Leu Ala Phe Ala Lys Glu Pro Phe Asp Ile Lys  
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Pro Gly Ala Cys Gly Thr Val Val Arg Asn Ala Glu Met Lys Ile Val  
355 360 365  
Asp Pro Glu Thr Gly Val Ser Leu Pro Arg Asn Gln Pro Gly Glu Ile  
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Cys Ile Arg Gly Asp Gln Ile Met Lys Gly Tyr Leu Asn Asp Pro Glu  
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Ala Thr Ser Arg Thr Ile Asp Lys Glu Gly Trp Leu His Thr Gly Asp  
405 410 415  
Ile Gly Tyr Ile Asp Asp Asp Asp Glu Leu Phe Ile Val Asp Arg Leu  
420 425 430  
Lys Glu Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala Pro Thr Glu Leu  
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Glu Ala Leu Leu Ile Ala His Pro Glu Ile Ser Asp Ala Ala Val Val  
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Gly Leu Lys Asp Glu Asp Ala Gly Glu Val Pro Val Ala Phe Val Val  
465 470 475 480  
Lys Ser Glu Lys Ser Gln Ala Thr Glu Asp Glu Ile Lys Gln Tyr Ile  
485 490 495  
Ser Lys Gln Val Ile Phe Tyr Lys Arg Ile Lys Arg Val Phe Phe Ile  
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20	25	30	
aga tca aaa cta cca gac ata acc atc tcg aac gac ctc cct ctg cac			144
Arg Ser Lys Leu Pro Asp Ile Thr Ile Ser Asn Asp Leu Pro Leu His			
35	40	45	
gca tac tgc ttt gaa aac ctc tct gat ttc tca gat agg cca tgc ttg			192
Ala Tyr Cys Phe Glu Asn Leu Ser Asp Phe Ser Asp Arg Pro Cys Leu			
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Ile Ser Gly Ser Thr Gly Lys Thr Tyr Ser Phe Ala Glu Thr His Leu			
65	70	75	80
ata tct cgg aag gtc gct ggt tta tcc aat ttg ggc atc aag aaa			288
Ile Ser Arg Lys Val Ala Ala Gly Leu Ser Asn Leu Gly Ile Lys Lys			
85	90	95	
ggc gat gta atc atg acc ctg ctc caa aac tgc cca gaa ttc gtc ttc			336
Gly Asp Val Ile Met Thr Leu Leu Gln Asn Cys Pro Glu Phe Val Phe			
100	105	110	
tcc ttc atc ggt gct tcc atg att ggt gca gtc atc acc act gcg aac			384
Ser Phe Ile Gly Ala Ser Met Ile Gly Ala Val Ile Thr Thr Ala Asn			
115	120	125	
cct ttc tac act caa agt gaa ata ttc aag caa ttc tct gct tct cgt			432
Pro Phe Tyr Thr Gln Ser Glu Ile Phe Lys Gln Phe Ser Ala Ser Arg			
130	135	140	
gcg aaa ctg att atc acc cag tct caa tat gtg aac aag cta gga gat			480
Ala Lys Leu Ile Ile Thr Gln Ser Gln Tyr Val Asn Lys Leu Gly Asp			
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agt gat tgc cat gaa aac aac caa aaa ccg ggg gaa gat ttc ata gta			528
Ser Asp Cys His Glu Asn Asn Gln Lys Pro Glu Asp Phe Ile Val			
165	170	175	
atc acc att gat gac ccg cca gag aac tgt cta cat ttc aat gtg ctt			576
Ile Thr Ile Asp Asp Pro Pro Glu Asn Cys Leu His Phe Asn Val Leu			

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gtc gag gct agc gag agt gaa atg cca aca gtt tca atc ctt ccg gat				624
Val Glu Ala Ser Glu Ser Glu Met Pro Thr Val Ser Ile Leu Pro Asp				
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Asp Pro Val Ala Leu Pro Phe Ser Ser Gly Thr Thr Gly Leu Pro Lys				
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gga gtg ata ctg acc cac aag agc ttg ata aca agt gtg gct caa caa				720
Gly Val Ile Leu Thr His Lys Ser Leu Ile Thr Ser Val Ala Gln Gln				
225	230		235	240
gtt gat gga gag atc cca aat tta tac ttg aaa caa gat gac gtt gtt				768
Val Asp Gly Glu Ile Pro Asn Leu Tyr Leu Lys Gln Asp Asp Val Val				
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Leu Cys Val Leu Pro Leu Phe His Ile Phe Ser Leu Asn Ser Val Leu				
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tta tgc tcg ttg aga gcc ggt tct gct gtt ctt tta atg caa aag ttt				864
Leu Cys Ser Leu Arg Ala Gly Ser Ala Val Leu Leu Met Gln Lys Phe				
275	280		285	
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Glu Ile Gly Ser Leu Leu Glu Leu Ile Gln Lys His Asn Val Ser Val				
290	295		300	
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Ala Ala Val Val Pro Pro Leu Val Leu Ala Leu Ala Lys Asn Pro Leu				
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Glu Ala Asn Phe Asp Leu Ser Ser Ile Arg Val Val Leu Ser Gly Ala				
325	330		335	
gcg cca ctg ggg aag gag ctc gag gac gcc ctc agg agc agg gtt cct				1056
Ala Pro Leu Gly Lys Glu Leu Glu Asp Ala Leu Arg Ser Arg Val Pro				
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Gln Ala Ile Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro Val				
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Leu Ser Met Cys Leu Ala Phe Ser Lys Gln Pro Phe Pro Thr Lys Ser				
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ggg tcg tgt gga acg gtg gtt aga aac gca gag ctc aag gtc att gac				1200
Gly Ser Cys Gly Thr Val Val Arg Asn Ala Glu Leu Lys Val Ile Asp				
385	390		395	400
cct gag acc ggt cgc tct ctt ggt tac aac caa cct ggt gaa atc tgc				1248
Pro Glu Thr Gly Arg Ser Leu Gly Tyr Asn Gln Pro Gly Glu Ile Cys				
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atc cgt gga tcc caa atc atg aaa gga tat ttg aat gac gcg gaa gcc				1296
Ile Arg Gly Ser Gln Ile Met Lys Gly Tyr Leu Asn Asp Ala Glu Ala				
420	425		430	

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Gly Tyr Val Asp Asp Asp Glu Ile Phe Ile Val Asp Arg Val Lys	
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gaa atc ata aaa ttc aaa ggc ttc cag gtg ccg cca gcg gag ctt gag	1440
Glu Ile Ile Lys Phe Lys Gly Phe Gln Val Pro Pro Ala Glu Leu Glu	
465 470 475 480	
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Ala Leu Leu Val Asn His Pro Ser Ile Ala Asp Ala Ala Val Val Pro	
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Gln Lys Asp Glu Val Ala Gly Glu Val Pro Val Ala Phe Val Val Arg	
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Ser Asp Asp Leu Asp Leu Ser Glu Glu Ala Val Lys Glu Tyr Ile Ala	
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Lys Gln Val Val Phe Tyr Lys Lys Leu His Lys Val Phe Phe Val His	
530 535 540	
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Ser Ile Pro Lys Ser Ala Ser Gly Lys Ile Leu Arg Lys Asp Leu Arg	
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Gly Asp Val Ile Met Thr Leu Leu Gln Asn Cys Pro Glu Phe Val Phe	
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Ser Asp Cys His Glu Asn Asn Gln Lys Pro Gly Glu Asp Phe Ile Val		160
165	170	175
Ile Thr Ile Asp Asp Pro Pro Glu Asn Cys Leu His Phe Asn Val Leu		
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195	200	205
Asp Pro Val Ala Leu Pro Phe Ser Ser Gly Thr Thr Gly Leu Pro Lys		
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Gly Val Ile Leu Thr His Lys Ser Leu Ile Thr Ser Val Ala Gln Gln		
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Val Asp Gly Glu Ile Pro Asn Leu Tyr Leu Lys Gln Asp Asp Val Val		240
245	250	255
Leu Cys Val Leu Pro Leu Phe His Ile Phe Ser Leu Asn Ser Val Leu		
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275	280	285
Glu Ile Gly Ser Leu Leu Glu Leu Ile Gln Lys His Asn Val Ser Val		
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Ala Ala Val Val Pro Pro Leu Val Leu Ala Leu Ala Lys Asn Pro Leu		
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Glu Ala Asn Phe Asp Leu Ser Ser Ile Arg Val Val Leu Ser Gly Ala		320
325	330	335
Ala Pro Leu Gly Lys Glu Leu Glu Asp Ala Leu Arg Ser Arg Val Pro		
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Leu Ser Met Cys Leu Ala Phe Ser Lys Gln Pro Phe Pro Thr Lys Ser		
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Gly Ser Cys Gly Thr Val Val Arg Asn Ala Glu Leu Lys Val Ile Asp		
385	390	395
Pro Glu Thr Gly Arg Ser Leu Gly Tyr Asn Gln Pro Gly Glu Ile Cys		400
405	410	415
Ile Arg Gly Ser Gln Ile Met Lys Gly Tyr Leu Asn Asp Ala Glu Ala		
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Thr Ala Asn Thr Ile Asp Val Glu Gly Trp Leu His Thr Gly Asp Ile		
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Gly Tyr Val Asp Asp Asp Asp Glu Ile Phe Ile Val Asp Arg Val Lys		
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Glu Ile Ile Lys Phe Lys Gly Phe Gln Val Pro Pro Ala Glu Leu Glu		
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Ala Leu Leu Val Asn His Pro Ser Ile Ala Asp Ala Ala Val Val Pro		
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Gln Lys Asp Glu Val Ala Gly Glu Val Pro Val Ala Phe Val Val Arg		
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Ser Asp Asp Leu Asp Leu Ser Glu Glu Ala Val Lys Glu Tyr Ile Ala		
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Lys Gln Val Val Phe Tyr Lys Lys Leu His Lys Val Phe Phe Val His		
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&lt;211&gt; 1172

&lt;212&gt; DNA

&lt;213&gt; Populus tremuloides Michx. (aspen)

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taattgggct	agatttaaca	gctattattc	aaactggcca	ggacaattat	taaaattaaat	660
aatttattat	ttttctaata	aagcacttcc	taattgttaa	aatatatgtc	taaacactaa	720
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gcataaaaata	taatggattt	gtggctgtt	aaaagacagg	tggaggacaa	gccacctctc	840
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ttaaatcaat	gtttcccta	tactaccccc	ccaaacaaactc	cataatacc	aatttgcct	1020
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<213> *Populus tremuloides* Michx. (aspen)

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